

SEQUENCE LISTING

<110> McCarthy, Sean A.

<120> NOVEL CRSP PROTEIN AND NUCLEIC ACID MOLECULES AND USES  
THEREFOR

<130> MEI-008

<140> 09/009,802  
<141> 1998-01-20

<150> 08/842,898  
<151> 1997-04-17

<150> 60/071,589  
<151> 1998-01-15

<160> 19

<170> PatentIn Ver. 2.0

<210> 1  
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<212> DNA  
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<220>  
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<222> (38)..(1087)

<220>  
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1 5

acc ctg ctg tgc ctg ctg gcg gcg gtc ccc acg gcc ccc gcg 103  
Thr Leu Leu Cys Leu Leu Ala Ala Ala Val Pro Thr Ala Pro Ala  
10 15 20

ccc gct ccg acg gcg acc tcg gct cca gtc aag ccc ggc ccg gct ctc 151  
Pro Ala Pro Thr Ala Thr Ser Ala Pro Val Lys Pro Gly Pro Ala Leu  
25 30 35

agc tac ccg cag gag gag gcc acc ctc aat gag atg ttc cgc gag gtt 199  
Ser Tyr Pro Gln Glu Ala Thr Leu Asn Glu Met Phe Arg Glu Val  
40 45 50

gag gaa ctg atg gag gac acg cag cac aaa ttg cgc agc gcg gtg gaa 247  
Glu Glu Leu Met Glu Asp Thr Gln His Lys Leu Arg Ser Ala Val Glu  
55 60 65 70

gag atg gag gca gaa gaa gct gct gct aaa gca tca tca gaa gtg aac	295
Glu Met Glu Ala Glu Glu Ala Ala Ala Lys Ala Ser Ser Glu Val Asn	
75 80 85	
ctg gca aac tta cct ccc agc tat cac aat gag acc aac aca gac acg	343
Leu Ala Asn Leu Pro Pro Ser Tyr His Asn Glu Thr Asn Thr Asp Thr	
90 95 100	
aac gtt gga aat aat acc atc cat gtg cac cga gaa att cac aag ata	391
Asn Val Gly Asn Asn Thr Ile His Val His Arg Glu Ile His Lys Ile	
105 110 115	
acc aac aac cag act gga caa atg gtc ttt tca gag aca gtt atc aca	439
Thr Asn Asn Gln Thr Gly Gln Met Val Phe Ser Glu Thr Val Ile Thr	
120 125 130	
tct gtg gga gac gaa gaa ggc aga agg agc cac gag tgc atc atc gac	487
Ser Val Gly Asp Glu Gly Arg Arg Ser His Glu Cys Ile Ile Asp	
135 140 145 150	
gag gac tgt ggg ccc agc atg tac tgc cag ttt gcc agc ttc cag tac	535
Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln Phe Ala Ser Phe Gln Tyr	
155 160 165	
acc tgc cag cca tgc cgg ggc cag agg atg ctc tgc acc cgg gac agt	583
Thr Cys Gln Pro Cys Arg Gly Gln Arg Met Leu Cys Thr Arg Asp Ser	
170 175 180	
gag tgc tgt gga gac cag ctg tgt gtc tgg ggt cac tgc acc aaa atg	631
Glu Cys Cys Gly Asp Gln Leu Cys Val Trp Gly His Cys Thr Lys Met	
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gcc acc agg ggc agc aat ggg acc atc tgt gac aac cag agg gac tgc	679
Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys Asp Asn Gln Arg Asp Cys	
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cag ccg ggg ctg tgc tgt gcc ttc cag aga ggc ctg ctg ttc cct gtg	727
Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg Gly Leu Leu Phe Pro Val	
215 220 225 230	
tgc aca ccc ctg ccc gtg gag ggc gag ctt tgc cat gac ccc gcc agc	775
Cys Thr Pro Leu Pro Val Glu Gly Glu Leu Cys His Asp Pro Ala Ser	
235 240 245	
cgg ctt ctg gac ctc atc acc tgg gag cta gag cct gat gga gcc ttg	823
Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu Glu Pro Asp Gly Ala Leu	
250 255 260	
gac cga tgc cct tgt gcc agt ggc ctc ctc tgc cag ccc cac agc cac	871
Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu Cys Gln Pro His Ser His	
265 270 275	
agc ctg gtg tat gtg tgc aag ccg acc ttc gtg ggg agc cgt gac caa	919
Ser Leu Val Tyr Val Cys Lys Pro Thr Phe Val Gly Ser Arg Asp Gln	
280 285 290	

B  
Cont.

gat ggg gag atc ctg ctg ccc aga gag gtc ccc gat gag tat gaa gtt 967  
Asp Gly Glu Ile Leu Leu Pro Arg Glu Val Pro Asp Glu Tyr Glu Val  
295 300 305 310

ggc agc ttc atg gag gag gtg cgc cag gag ctg gag gac ctg gag agg 1015  
Gly Ser Phe Met Glu Glu Val Arg Gln Glu Leu Glu Asp Leu Glu Arg  
315 320 325

agc ctg act gaa gag atg gcg ctg agg gag cct gcg gct gcc gcc gct 1063  
Ser Leu Thr Glu Glu Met Ala Leu Arg Glu Pro Ala Ala Ala Ala  
330 335 340

gca ctg ctg gga agg gaa gag att tagatctgga ccaggctgtg ggttagatgtg 1117  
Ala Leu Leu Gly Arg Glu Glu Ile  
345 350

caatagaaaat agctaattta tttccccang ttgtgtcttt aagcgtgggc tgaccaggct 1177  
tcttcctaca tcttcttccc agtaagttc ccctctggct tgacagcatg aggtgttgc 1237  
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ggcgaggatt ataaatgaaa tttgcaaaat cacttagcag caactgaaga caattatcaa 2197  
ccacgtggag aaaatcaaac cgagcagggc tgggtgaaac atgggtgtaa tatgcgactg 2257  
cgaacactga actctacgccc actccacaaa tggatgttttc aggtgtcatg gactgttgcc 2317

B  
Cont.

accatgtatt catccagagt tcttaaagtt taaagttgca catgattgta taagcatgct 2377  
ttcttgagt tttaaattat gtataaacat aagttgcatt tagaaatcaa gcataaatca 2437  
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<212> PRT  
<213> Homo sapiens

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Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn  
35 40 45  
Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys  
50 55 60  
Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys  
65 70 75 80  
Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn  
85 90 95  
Glu Thr Asn Thr Asp Thr Asn Val Gly Asn Asn Thr Ile His Val His  
100 105 110  
Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe  
115 120 125  
Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser  
130 135 140  
His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln  
145 150 155 160  
Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met  
165 170 175  
Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp  
180 185 190  
Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys  
195 200 205  
Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg  
210 215 220

B  
B  
C  
C  
T

Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu  
225 230 235 240

Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu  
245 250 255

Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu  
260 265 270

Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe  
275 280 285

Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg Glu Val  
290 295 300

Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu  
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gtc ccc acg gcc ccc gcg ccc gct ccg acg gcg acc tcg gct cca gtc 96  
Val Pro Thr Ala Pro Ala Pro Ala Pro Thr Ala Thr Ser Ala Pro Val  
20 25 30

aag ccc ggc ccg gct ctc acg tac ccg cag gag gag gcc acc ctc aat 144  
Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn  
35 40 45

gag atg ttc cgc gag gtt gag gaa ctg atg gag gac acg cag cac aaa 192  
Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys  
50 55 60

ttg cgc acg gcg gtg gaa gag atg gag gca gaa gaa gct gct gct aaa 240  
Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys  
65 70 75 80

B1  
CMT.

gca tca tca gaa gtg aac ctg gca aac tta cct ccc agc tat cac aat Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn 85 90 95	288
gag acc aac aca gac acg aac gtt gga aat aat acc atc cat gtg cac Glu Thr Asn Thr Asp Thr Asn Val Gly Asn Asn Thr Ile His Val His 100 105 110	336
cga gaa att cac aag ata acc aac aac cag act gga caa atg gtc ttt Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe 115 120 125	384
tca gag aca gtt atc aca tct gtg gga gac gaa ggc aga agg agc Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser 130 135 140	432
cac gag tgc atc atc gac gag gac tgt ggg ccc agc atg tac tgc cag His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln 145 150 155 160	480
ttt gcc agc ttc cag tac acc tgc cag cca tgc cgg ggc cag agg atg Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met 165 170 175	528
ctc tgc acc cgg gac agt gag tgc tgt gga gac cag ctg tgt gtc tgg Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp 180 185 190	576
ggc cac tgc acc aaa atg gcc acc agg ggc agc aat ggg acc atc tgt Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys 195 200 205	624
gac aac cag agg gac tgc cag ccg ggg ctg tgc tgt gcc ttc cag aga Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg 210 215 220	672
ggc ctg ctg ttc cct gtg tgc aca ccc ctg ccc gtg gag ggc gag ctt Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu 225 230 235 240	720
tgc cat gac ccc gcc agc cgg ctt ctg gac ctc atc acc tgg gag cta Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu 245 250 255	768
gag cct gat gga gcc ttg gac cga tgc cct tgt gcc agt ggc ctc ctc Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu 260 265 270	816
tgc cag ccc cac agc cac agc ctg gtg tat gtg tgc aag ccg acc ttc Cys Gln Pro His Ser His Leu Val Tyr Val Cys Lys Pro Thr Phe 275 280 285	864
gtg ggg agc cgt gac caa gat ggg gag atc ctg ctg ccc aga gag gtc Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg Glu Val 290 295 300	912

B  
Cmt

ccc gat gag tat gaa gtt ggc agc ttc atg gag gag gtg cgc cag gag 960  
Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu  
305 310 315 320

ctg gag gac ctg gag agg agc ctg act gaa gag atg gcg ctg agg gag 1008  
Leu Glu Asp Leu Glu Arg Ser Leu Thr Glu Glu Met Ala Leu Arg Glu  
325 330 335

cct gcg gct gcc gct gca ctg ctg gga agg gaa gag att 1050  
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aagg atg gtg gcg gcc gtc ctg ctg ggg ctg agc tgg ctc tgc tct ccc 169  
Met Val Ala Ala Val Leu Leu Gly Leu Ser Trp Leu Cys Ser Pro  
1 5 10 15

ctg gga gct ctg gtc ctg gac ttc aac aac atc agg agc tct gct gac 217  
Leu Gly Ala Leu Val Leu Asp Phe Asn Asn Ile Arg Ser Ser Ala Asp  
20 25 30

ctg cat ggg gcc cgg aag ggc tca cag tgc ctg tct gac acg gac tgc 265  
Leu His Gly Ala Arg Lys Gly Ser Gln Cys Leu Ser Asp Thr Asp Cys  
35 40 45

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*Cont.*  
aat acc aga aag ttc tgc ctc cag ccc cgc gat gag aag ccg ttc tgt 313  
Asn Thr Arg Lys Phe Cys Leu Gln Pro Arg Asp Glu Lys Pro Phe Cys  
50 55 60

gct aca tgt cgt ggg ttg cgg agg agg tgc cag cga gat gcc atg tgc 361  
Ala Thr Cys Arg Gly Leu Arg Arg Cys Gln Arg Asp Ala Met Cys  
65 70 75

tgc cct ggg aca ctc tgt gtg aac gat gtt tgt act acg atg gaa gat 409  
Cys Pro Gly Thr Leu Cys Val Asn Asp Val Cys Thr Thr Met Glu Asp  
80 85 90 95

gca acc cca ata tta gaa agg cag ctt gat gag caa gat ggc aca cat 457  
Ala Thr Pro Ile Leu Glu Arg Gln Leu Asp Glu Gln Asp Gly Thr His  
100 105 110

gca gaa gga aca act ggg cac cca gtc cag gaa aac caa ccc aaa agg		505	
Ala Glu Gly Thr Thr Gly His Pro Val Gln Glu Asn Gln Pro Lys Arg			
115	120	125	
aag cca agt att aag aaa tca caa ggc agg aag gga caa gag gga gaa		553	
Lys Pro Ser Ile Lys Lys Ser Gln Gly Arg Lys Gly Gln Glu Gly Glu			
130	135	140	
agt tgt ctg aga act ttt gac tgt ggc cct gga ctt tgc tgt gct cgt		601	
Ser Cys Leu Arg Thr Phe Asp Cys Gly Pro Gly Leu Cys Cys Ala Arg			
145	150	155	
cat ttt tgg acg aaa att tgt aag cca gtc ctt ttg gag gga cag gtc		649	
His Phe Trp Thr Lys Ile Cys Lys Pro Val Leu Leu Glu Gly Gln Val			
160	165	170	175
tgc tcc aga aga ggg cat aaa gac act gct caa gct cca gaa atc ttc		697	
Cys Ser Arg Arg Gly His Lys Asp Thr Ala Gln Ala Pro Glu Ile Phe			
180	185	190	
cag cgt tgc gac tgt ggc cct gga cta ctg tgt cga agc caa ttg acc		745	
Gln Arg Cys Asp Cys Gly Pro Gly Leu Leu Cys Arg Ser Gln Leu Thr			
195	200	205	
agc aat cgg cag cat gct cga tta aga gta tgc caa aaa ata gaa aag		793	
Ser Asn Arg Gln His Ala Arg Leu Arg Val Cys Gln Lys Ile Glu Lys			
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Leu			

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His Gly Ala Arg Lys Gly Ser Gln Cys Leu Ser Asp Thr Asp Cys Asn			
35	40	45	
Thr Arg Lys Phe Cys Leu Gln Pro Arg Asp Glu Lys Pro Phe Cys Ala			
50	55	60	
Thr Cys Arg Gly Leu Arg Arg Cys Gln Arg Asp Ala Met Cys Cys			
65	70	75	80
Pro Gly Thr Leu Cys Val Asn Asp Val Cys Thr Thr Met Glu Asp Ala			
85	90	95	

Thr Pro Ile Leu Glu Arg Gln Leu Asp Glu Gln Asp Gly Thr His Ala  
100 105 110

Glu Gly Thr Thr Gly His Pro Val Gln Glu Asn Gln Pro Lys Arg Lys  
115 120 125

Pro Ser Ile Lys Lys Ser Gln Gly Arg Lys Gly Gln Glu Gly Glu Ser  
130 135 140

Cys Leu Arg Thr Phe Asp Cys Gly Pro Gly Leu Cys Cys Ala Arg His  
145 150 155 160

Phe Trp Thr Lys Ile Cys Lys Pro Val Leu Leu Glu Gly Gln Val Cys  
165 170 175

Ser Arg Arg Gly His Lys Asp Thr Ala Gln Ala Pro Glu Ile Phe Gln  
180 185 190

Arg Cys Asp Cys Gly Pro Gly Leu Leu Cys Arg Ser Gln Leu Thr Ser  
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gga gct ctg gtc ctg gac ttc aac aac atc agg agc tct gct gac ctg 96  
Gly Ala Leu Val Leu Asp Phe Asn Asn Ile Arg Ser Ser Ala Asp Leu  
20 25 30

cat ggg gcc cgg aag ggc tca cag tgc ctg tct gac acg gac tgc aat 144  
His Gly Ala Arg Lys Gly Ser Gln Cys Leu Ser Asp Thr Asp Cys Asn  
35 40 45

acc aga aag ttc tgc ctc cag ccc cgc gat gag aag ccg ttc tgt gct 192  
Thr Arg Lys Phe Cys Leu Gln Pro Arg Asp Glu Lys Pro Phe Cys Ala  
50 55 60

aca tgt cgt ggg ttg cgg agg agg tgc cag cga gat gcc atg tgc tgc 240  
Thr Cys Arg Gly Leu Arg Arg Cys Gln Arg Asp Ala Met Cys Cys  
65 70 75 80

B  
Cont.

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															95	
acc	cca	ata	tta	gaa	agg	cag	ctt	gat	gag	caa	gat	ggc	aca	cat	gca	336
Thr	Pro	Ile	Leu	Glu	Arg	Gln	Leu	Asp	Glu	Gln	Asp	Gly	Thr	His	Ala	
															110	
gaa	gga	aca	act	ggg	cac	cca	gtc	cag	gaa	aac	caa	ccc	aaa	agg	aag	384
Glu	Gly	Thr	Thr	Gly	His	Pro	Val	Gln	Glu	Asn	Gln	Pro	Lys	Arg	Lys	
															125	
cca	agt	att	aag	aaa	tca	caa	ggc	agg	aag	gga	caa	gag	gga	gaa	agt	432
Pro	Ser	Ile	Lys	Lys	Ser	Gln	Gly	Arg	Lys	Gly	Gln	Glu	Gly	Glu	Ser	
															140	
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Cys	Leu	Arg	Thr	Phe	Asp	Cys	Gly	Pro	Gly	Leu	Cys	Cys	Ala	Arg	His	
															160	
ttt	tgg	acg	aaa	att	tgt	aag	cca	gtc	ctt	ttg	gag	gga	cag	gtc	tgc	528
Phe	Trp	Thr	Lys	Ile	Cys	Lys	Pro	Val	Leu	Leu	Glu	Gly	Gln	Val	Cys	
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tcc	aga	aga	ggg	cat	aaa	gac	act	gct	caa	gct	cca	gaa	atc	ttc	cag	576
Ser	Arg	Arg	Gly	His	Lys	Asp	Thr	Ala	Gln	Ala	Pro	Glu	Ile	Phe	Gln	
															190	
cgt	tgc	gac	tgt	ggc	cct	gga	cta	ctg	tgt	cga	agc	caa	ttg	acc	agc	624
Arg	Cys	Asp	Cys	Gly	Pro	Gly	Leu	Leu	Cys	Arg	Ser	Gln	Leu	Thr	Ser	
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aat	cgg	cag	cat	gct	cga	tta	aga	gtt	tgc	caa	aaa	ata	gaa	aag	cta	672
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*ant.*

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<222> (93)..(890)

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						Met	Met	Ala	Leu	Gly	Ala	Ala					
						1				5							
gga	gct	acc	cg	gtc	ttt	gtc	g	atg	gta	g	g	161					
Gly	Ala	Thr	Arg	Val	Phe	Val	Ala	Met	Val	Ala	Ala	Leu	Gly	Gly			
10							15			20							
cac	cct	ctg	ctg	gga	gtg	agc	gcc	acc	ttg	aa	tcg	gt	ctc	aat	tcc	209	
His	Pro	Leu	Leu	Gly	Val	Ser	Ala	Thr	Leu	Asn	Ser	Val	Leu	Asn	Ser		
25							30			35							
aac	gct	atc	aag	aa	ctg	ccc	cca	ccg	ctg	ggc	ggc	gct	g	cg	gg	257	
Asn	Ala	Ile	Lys	Asn	Leu	Pro	Pro	Pro	Leu	Gly	Gly	Ala	Ala	Gly	His		
40							45			50			55				
cca	ggc	tct	gca	gtc	agc	gcc	g	cg	gga	atc	ctg	ta	ccg	ggc	gg	305	
Pro	Gly	Ser	Ala	Val	Ser	Ala	Ala	Pro	Gly	Ile	Leu	Tyr	Pro	Gly	Gly		
60							65			70							
aat	aag	ta	cag	ac	att	gac	aa	ta	cag	ccg	ta	ccg	tg	ca	ga	353	
Asn	Lys	Tyr	Gln	Thr	Ile	Asp	Asn	Tyr	Gln	Pro	Tyr	Pro	Cys	Ala	Glu		
75							80			85							
gac	gag	gag	tgc	ggc	act	gat	gag	ta	tc	g	ct	g	cc	ac	cg	gg	401
Asp	Glu	Glu	Cys	Gly	Thr	Asp	Glu	Tyr	Cys	Ala	Ser	Pro	Thr	Arg	Gly		
90							95			100							
ggg	gac	gca	ggc	gtg	caa	atc	tgt	ctc	gcc	tgc	agg	aag	cg	cg	aaa	449	
Gly	Asp	Ala	Gly	Val	Gln	Ile	Cys	Leu	Ala	Cys	Arg	Lys	Arg	Arg	Lys		
105							110			115							
cgc	tgc	atg	cgt	cac	gct	atg	tgc	ccc	ggg	aat	ta	tc	aa	aa	aa	497	
Arg	Cys	Met	Arg	His	Ala	Met	Cys	Cys	Pro	Gly	Asn	Tyr	Cys	Lys	Asn		
120							125			130			135				
gga	ata	tgc	gtg	tct	tct	gat	caa	aa	at	ca	tg	ca	gg	aa	tt	gag	545
Gly	Ile	Cys	Val	Ser	Ser	Asp	Gln	Asn	His	Phe	Arg	Gly	Gl	Ile	Gl		
140							145			150							
gaa	acc	atc	act	gaa	agc	ttt	ggt	aat	gat	ca	tg	ca	gg	aa	tt	gag	593
Glu	Thr	Ile	Thr	Glu	Ser	Phe	Gly	Asn	Asp	His	Ser	Thr	Leu	Asp	Gly		
155							160			165							
tat	tcc	aga	aga	acc	acc	ttg	tct	tca	aaa	atg	tat	cac	acc	aa	gg	641	
Tyr	Ser	Arg	Arg	Thr	Thr	Leu	Ser	Ser	Lys	Met	Tyr	His	Thr	Lys	Gly		
170							175			180							
caa	gaa	gg	tct	tgt	tgt	ctc	cg	tca	tca	gac	tgt	ggc	tca	gg	tt	689	
Gln	Glu	Gly	Ser	Val	Cys	Leu	Arg	Ser	Ser	Asp	Cys	Ala	Ser	Gly	Leu		
185							190			195							
tgt	tgt	gct	aga	cac	ttc	tgg	tcc	aag	atc	tgt	aaa	cct	gtc	ctg	aa	737	
Cys	Cys	Ala	Arg	His	Phe	Trp	Ser	Lys	Ile	Cys	Lys	Pro	Val	Leu	Lys		
200							205			210			215				

B  
Cont

gaa ggt caa gtg tgt acc aag cat agg aga aaa ggc tct cat gga cta 785  
Glu Gly Gln Val Cys Thr Lys His Arg Arg Lys Gly Ser His Gly Leu  
220 225 230

gaa ata ttc cag cgt tgt tac tgt gga gaa ggt ctg tct tgc cgg ata 833  
Glu Ile Phe Gln Arg Cys Tyr Cys Gly Glu Gly Leu Ser Cys Arg Ile  
235 240 245

cag aaa gat cac cat caa gcc agt aat tct tct agg ctt cac act tgt 881  
Gln Lys Asp His His Gln Ala Ser Asn Ser Ser Arg Leu His Thr Cys  
250 255 260

cag aga cac taaaccagct atccaaaatg cagtgaactc cttttatata 930  
Gln Arg His  
265

atagatgcta tgaaaacctt ttatgacctt catcaactca atcctaagga tatacaagtt 990  
ctgtggtttc agttaagcat tccaataaca cttccaaaa acctggagtg taagagcttt 1050  
gtttcttat ggaactcccc tgtgattgca gtaaattact gtattgtaaa ttctcagtg 1110  
ggcacttacc tgtaaatgca atgaaacttt taattatttt tctaaagggtg ctgcactgcc 1170  
tattttcctt cttgttatgt aaattttgt acacattgtat tgttatctt actgacaaat 1230  
attctatattt gaactgaagt aaatcatttc agcttatagt tctaaaagc ataacccttt 1290  
accccattnn attctagagt cnagaacgca aggtctt ggaatgacaa atgataggt 1350  
cctaaaaatgt aacatgaaaa tactagctt tttctgaaa tgtactatct taatgcttaa 1410  
attatatttc cctttaggtgt gtagatgttt ttgaaataaa atttaacatt taatatcatg 1470  
aaatgkata agtagacata aaaaaaaaaa aaaaaaaaaa agggcggccg ctagactag 1529

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<210> 8  
<211> 266  
<212> PRT  
<213> Homo sapiens

<400> 8  
Met Met Ala Leu Gly Ala Ala Gly Ala Thr Arg Val Phe Val Ala Met  
1 5 10 15

Val Ala Ala Ala Leu Gly Gly His Pro Leu Leu Gly Val Ser Ala Thr  
20 25 30

Leu Asn Ser Val Leu Asn Ser Asn Ala Ile Lys Asn Leu Pro Pro Pro  
35 40 45

Leu Gly Gly Ala Ala Gly His Pro Gly Ser Ala Val Ser Ala Ala Pro  
50 55 60

Gly Ile Leu Tyr Pro Gly Gly Asn Lys Tyr Gln Thr Ile Asp Asn Tyr  
65 70 75 80

Gln Pro Tyr Pro Cys Ala Glu Asp Glu Glu Cys Gly Thr Asp Glu Tyr  
85 90 95

Cys Ala Ser Pro Thr Arg Gly Gly Asp Ala Gly Val Gln Ile Cys Leu  
100 105 110

Ala Cys Arg Lys Arg Arg Lys Arg Cys Met Arg His Ala Met Cys Cys  
115 120 125

Pro Gly Asn Tyr Cys Lys Asn Gly Ile Cys Val Ser Ser Asp Gln Asn  
130 135 140

His Phe Arg Gly Glu Ile Glu Glu Thr Ile Thr Glu Ser Phe Gly Asn  
145 150 155 160

Asp His Ser Thr Leu Asp Gly Tyr Ser Arg Arg Thr Thr Leu Ser Ser  
165 170 175

Lys Met Tyr His Thr Lys Gly Gln Glu Gly Ser Val Cys Leu Arg Ser  
180 185 190

Ser Asp Cys Ala Ser Gly Leu Cys Cys Ala Arg His Phe Trp Ser Lys  
195 200 205

Ile Cys Lys Pro Val Leu Lys Glu Gly Gln Val Cys Thr Lys His Arg  
210 215 220

Arg Lys Gly Ser His Gly Leu Glu Ile Phe Gln Arg Cys Tyr Cys Gly  
225 230 235 240

Glu Gly Leu Ser Cys Arg Ile Gln Lys Asp His His Gln Ala Ser Asn  
245 250 255

Ser Ser Arg Leu His Thr Cys Gln Arg His  
260 265

B1  
CANT  
<210> 9  
<211> 798  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)..(798)

<400> 9  
atg atg gct ctg ggc gca gcg gga gct acc cgg gtc ttt gtc gcg atg 48  
Met Met Ala Leu Gly Ala Ala Gly Ala Thr Arg Val Phe Val Ala Met  
1 5 10 15

gta gcg gcg gct ctc ggc ggc cac cct ctg ctg gga gtg agc gcc acc	96
Val Ala Ala Ala Leu Gly Gly His Pro Leu Leu Gly Val Ser Ala Thr	
20 25 30	
ttg aac tcg gtt ctc aat tcc aac gct atc aag aac ctg ccc cca ccg	144
Leu Asn Ser Val Leu Asn Ser Asn Ala Ile Lys Asn Leu Pro Pro Pro	
35 40 45	
ctg ggc ggc gct gcg ggg cac cca ggc tct gca gtc agc gcc gcg ccg	192
Leu Gly Gly Ala Ala Gly His Pro Gly Ser Ala Val Ser Ala Ala Pro	
50 55 60	
gga atc ctg tac ccg ggc ggg aat aag tac cag acc att gac aac tac	240
Gly Ile Leu Tyr Pro Gly Gly Asn Lys Tyr Gln Thr Ile Asp Asn Tyr	
65 70 75 80	
cag ccg tac ccg tgc gca gag gac gag gag tgc ggc act gat gag tac	288
Gln Pro Tyr Pro Cys Ala Glu Asp Glu Glu Cys Gly Thr Asp Glu Tyr	
85 90 95	
tgc gct agt ccc acc cgc gga ggg gac gca ggc gtg caa atc tgt ctc	336
Cys Ala Ser Pro Thr Arg Gly Gly Asp Ala Gly Val Gln Ile Cys Leu	
100 105 110	
gcc tgc agg aag cgc cga aaa cgc tgc atg cgt cac gct atg tgc tgc	384
Ala Cys Arg Lys Arg Arg Lys Arg Cys Met Arg His Ala Met Cys Cys	
115 120 125	
ccc ggg aat tac tgc aaa aat gga ata tgc gtg tct tct gat caa aat	432
Pro Gly Asn Tyr Cys Lys Asn Gly Ile Cys Val Ser Ser Asp Gln Asn	
130 135 140	
cat ttc cga gga gaa att gag gaa acc atc act gaa agc ttt ggt aat	480
His Phe Arg Gly Glu Ile Glu Glu Thr Ile Thr Glu Ser Phe Gly Asn	
145 150 155 160	
gat cat agc acc ttg gat ggg tat tcc aga aga acc acc ttg tct tca	528
Asp His Ser Thr Leu Asp Gly Tyr Ser Arg Arg Thr Thr Leu Ser Ser	
165 170 175	
aaa atg tat cac acc aaa gga caa gaa ggt tct gtt tgt ctc cgg tca	576
Lys Met Tyr His Thr Lys Gly Gln Glu Gly Ser Val Cys Leu Arg Ser	
180 185 190	
tca gac tgt gcc tca gga ttg tgt tgt gct aga cac ttc tgg tcc aag	624
Ser Asp Cys Ala Ser Gly Leu Cys Cys Ala Arg His Phe Trp Ser Lys	
195 200 205	
atc tgt aaa cct gtc ctg aaa gaa ggt caa gtg tgt acc aag cat agg	672
Ile Cys Lys Pro Val Leu Lys Glu Gly Gln Val Cys Thr Lys His Arg	
210 215 220	
aga aaa ggc tct cat gga cta gaa ata ttc cag cgt tgt tac tgt gga	720
Arg Lys Gly Ser His Gly Leu Glu Ile Phe Gln Arg Cys Tyr Cys Gly	
225 230 235 240	

B  
Cont.

gaa ggt ctg tct tgc cgg ata cag aaa gat cac cat caa gcc agt aat 768  
Glu Gly Leu Ser Cys Arg Ile Gln Lys Asp His His Gln Ala Ser Asn  
245 250 255

tct tct agg ctt cac act tgt cag aga cac 798  
Ser Ser Arg Leu His Thr Cys Gln Arg His  
260 265

<210> 10  
<211> 702  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)..(537)

<400> 10  
gaa ttc ggc acg agg gtt ggg agg tat tgc cac agt ccc cac caa gga 48  
Glu Phe Gly Thr Arg Val Gly Arg Tyr Cys His Ser Pro His Gln Gly  
1 5 10 15

tca tcg gcc tgc atg gtg tgt cgg aga aaa aag aag cgc tgc cac cga 96  
Ser Ser Ala Cys Met Val Cys Arg Arg Lys Lys Lys Arg Cys His Arg  
20 25 30

gat ggc atg tgc tgc ccc agt acc cgc tgc aat aat ggc atc tgt atc 144  
Asp Gly Met Cys Cys Pro Ser Thr Arg Cys Asn Asn Gly Ile Cys Ile  
35 40 45

cca gtt act gaa agc atc tta acc cct cac atc ccg gct ctg gat ggt 192  
Pro Val Thr Glu Ser Ile Leu Thr Pro His Ile Pro Ala Leu Asp Gly  
50 55 60

act cgg cac aga gat cga aac cac ggt cat tac tca aac cat gac ttg 240  
Thr Arg His Arg Asp Arg Asn His Gly His Tyr Ser Asn His Asp Leu  
65 70 75 80

gga tgg cag aat cta gga aga cca cac act aag atg tca cat ata aaa 288  
Gly Trp Gln Asn Leu Gly Arg Pro His Thr Lys Met Ser His Ile Lys  
85 90 95

ggg cat gaa gga gac ccc tgc cta cga tca tca gac tgc att gaa ggg 336  
Gly His Glu Gly Asp Pro Cys Leu Arg Ser Ser Asp Cys Ile Glu Gly  
100 105 110

ttt tgc tgt gct cgt cat ttc tgg acc aaa atc tgc aaa cca gtg ctc 384  
Phe Cys Cys Ala Arg His Phe Trp Thr Lys Ile Cys Lys Pro Val Leu  
115 120 125

cat cag ggg gaa gtc tgt acc aaa caa cgc aag aag ggt tct cat ggg 432  
His Gln Gly Glu Val Cys Thr Lys Gln Arg Lys Lys Gly Ser His Gly  
130 135 140

B  
Cont

ctg gaa att ttc cag cgt tgc gac tgt gcg aag ggc ctg tct tgc aaa 480  
Leu Glu Ile Phe Gln Arg Cys Asp Cys Ala Lys Gly Leu Ser Cys Lys  
145 150 155 160

gta tgg aaa gat gcc acc tac tcc tcc aaa gcc aga ctc cat gtg tgt 528  
Val Trp Lys Asp Ala Thr Tyr Ser Ser Lys Ala Arg Leu His Val Cys  
165 170 175

cag aaa att tgatcaccat tgaggaacat catcaattgc agactgtgaa 577  
Gln Lys Ile

gttgtgtatt taatgcatta tagcatggtg gaaaataagg ttcagatgca gaagaatggc 637  
taaaataaga aacgtgataa gaatatacat gatcacaaaa aaaaaaaaaaaa aaaagatgca 697  
ggcgc 702

<210> 11  
<211> 179  
<212> PRT  
<213> Homo sapiens

<400> 11  
Glu Phe Gly Thr Arg Val Gly Arg Tyr Cys His Ser Pro His Gln Gly  
1 5 10 15

Ser Ser Ala Cys Met Val Cys Arg Arg Lys Lys Lys Arg Cys His Arg  
20 25 30

Asp Gly Met Cys Cys Pro Ser Thr Arg Cys Asn Asn Gly Ile Cys Ile  
35 40 45

Pro Val Thr Glu Ser Ile Leu Thr Pro His Ile Pro Ala Leu Asp Gly  
50 55 60

Thr Arg His Arg Asp Arg Asn His Gly His Tyr Ser Asn His Asp Leu  
65 70 75 80

Gly Trp Gln Asn Leu Gly Arg Pro His Thr Lys Met Ser His Ile Lys  
85 90 95

Gly His Glu Gly Asp Pro Cys Leu Arg Ser Ser Asp Cys Ile Glu Gly  
100 105 110

Phe Cys Cys Ala Arg His Phe Trp Thr Lys Ile Cys Lys Pro Val Leu  
115 120 125

His Gln Gly Glu Val Cys Thr Lys Gln Arg Lys Lys Gly Ser His Gly  
130 135 140

Leu Glu Ile Phe Gln Arg Cys Asp Cys Ala Lys Gly Leu Ser Cys Lys  
145 150 155 160

Val Trp Lys Asp Ala Thr Tyr Ser Ser Lys Ala Arg Leu His Val Cys  
165 170 175

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Gln Lys Ile

<210> 12

<211> 537

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(537)

<400> 12

gaa ttc ggc acg agg gtt ggg agg tat tgc cac agt ccc cac caa gga	48
Glu Phe Gly Thr Arg Val Gly Arg Tyr Cys His Ser Pro His Gln Gly	
1 5 10 15	

tca tcg gcc tgc atg gtg tgt cgg aga aaa aag aag cgc tgc cac cga	96
Ser Ser Ala Cys Met Val Cys Arg Arg Lys Lys Lys Arg Cys His Arg	
20 25 30	

gat ggc atg tgc tgc ccc agt acc cgc tgc aat aat ggc atc tgt atc	144
Asp Gly Met Cys Cys Pro Ser Thr Arg Cys Asn Asn Gly Ile Cys Ile	
35 40 45	

cca gtt act gaa agc atc tta acc cct cac atc ccg gct ctg gat ggt	192
Pro Val Thr Glu Ser Ile Leu Thr Pro His Ile Pro Ala Leu Asp Gly	
50 55 60	

act cgg cac aga gat cga aac cac ggt cat tac tca aac cat gac ttg	240
Thr Arg His Arg Asp Arg Asn His Gly His Tyr Ser Asn His Asp Leu	
65 70 75 80	

gga tgg cag aat cta gga aga cca cac act aag atg tca cat ata aaa	288
Gly Trp Gln Asn Leu Gly Arg Pro His Thr Lys Met Ser His Ile Lys	
85 90 95	

ggg cat gaa gga gac ccc tgc cta cga tca tca gac tgc att gaa ggg	336
Gly His Glu Gly Asp Pro Cys Leu Arg Ser Ser Asp Cys Ile Glu Gly	
100 105 110	

ttt tgc tgt gct cgt cat ttc tgg acc aaa atc tgc aaa cca gtg ctc	384
Phe Cys Cys Ala Arg His Phe Trp Thr Lys Ile Cys Lys Pro Val Leu	
115 120 125	

cat cag ggg gaa gtc tgt acc aaa caa cgc aag aag ggt tct cat ggg	432
His Gln Gly Glu Val Cys Thr Lys Gln Arg Lys Lys Gly Ser His Gly	
130 135 140	

ctg gaa att ttc cag cgt tgc gac tgt gcg aag ggc ctg tct tgc aaa	480
Leu Glu Ile Phe Gln Arg Cys Asp Cys Ala Lys Gly Leu Ser Cys Lys	
145 150 155 160	

B  
Cont

gta tgg aaa gat gcc acc tac tcc tcc aaa gcc aga ctc cat gtg tgt 528  
Val Trp Lys Asp Ala Thr Tyr Ser Ser Lys Ala Arg Leu His Val Cys  
165 170 175

cag aaa att 537  
Gln Lys Ile

<210> 13  
<211> 928  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (75)...(800)

<400> 13  
ctcgaggcca aaattcggca cgaggccggg ctgtggtcta gcataaaggc ggagcccaga 60

agaagggcg gggatg gga gaa gcc tcc cca cct gcc ccc gca agg cgg 110  
Met Gly Ala Ser Pro Pro Ala Pro Ala Arg Arg  
1 5 10

cat ctg ctg gtc ctg ctg ctc ctc tct acc ctg gtg atc ccc tcc 158  
His Leu Leu Val Leu Leu Leu Ser Thr Leu Val Ile Pro Ser  
15 20 25

gct gca gct cct atc cat gat gct gac gcc caa gag agc tcc ttg ggt 206  
Ala Ala Ala Pro Ile His Asp Ala Asp Ala Gln Glu Ser Ser Leu Gly  
30 35 40

ctc aca ggc ctc cag agc cta ctc caa ggc ttc agc cga ctt ttc ctg 254  
Leu Thr Gly Leu Gln Ser Leu Leu Gln Gly Phe Ser Arg Leu Phe Leu  
45 50 55 60

aaa ggt aac ctg ctt cgg ggc ata gac agc tta ttc tct gcc ccc atg 302  
Lys Gly Asn Leu Leu Arg Gly Ile Asp Ser Leu Phe Ser Ala Pro Met  
65 70 75

gac ttc cgg ggc ctc cct ggg aac tac cac aaa gag gag aac cag gag 350  
Asp Phe Arg Gly Leu Pro Gly Asn Tyr His Lys Glu Glu Asn Gln Glu  
80 85 90

cac cag ctg ggg aac aac acc ctc tcc agc cac ctc cag atc gac aag 398  
His Gln Leu Gly Asn Asn Thr Leu Ser Ser His Leu Gln Ile Asp Lys  
95 100 105

atg acc gac aac aag aca gga gag gtg ctg atc tcc gag aat gtg gtg 446  
Met Thr Asp Asn Lys Thr Gly Glu Val Leu Ile Ser Glu Asn Val Val  
110 115 120

gca tcc att caa cca gcg gag ggg agc ttc gag ggt gat ttg aag gta 494  
Ala Ser Ile Gln Pro Ala Glu Gly Ser Phe Glu Gly Asp Leu Lys Val  
125 130 135 140

ccc agg atg gag gag aag gag gcc ctg gta ccc atc cag aag gcc acg 542  
Pro Arg Met Glu Glu Lys Glu Ala Leu Val Pro Ile Gln Lys Ala Thr  
145 150 155

gac agc ttc cac aca gaa ctc cat ccc cggtg gcc ttc tgg atc att 590  
Asp Ser Phe His Thr Glu Leu His Pro Arg Val Ala Phe Trp Ile Ile  
160 165 170

aag ctg cca cggtg agg tcc cac cag gat gcc ctg gag ggc ggc cac 638  
Lys Leu Pro Arg Arg Ser His Gln Asp Ala Leu Glu Gly Gly His  
175 180 185

tgg ctc agc gag aag cga cac cggtg cag gcc atc cggtg gat gga ctc 686  
Trp Leu Ser Glu Lys Arg His Arg Leu Gln Ala Ile Arg Asp Gly Leu  
190 195 200

cgc aag ggg acc cac aag gac gtc cta gaa gag ggg acc gag agc tcc 734  
Arg Lys Gly Thr His Lys Asp Val Leu Glu Gly Thr Glu Ser Ser  
205 210 215 220

tcc cac tcc agg ctg tcc ccc cga aag acc cac tta ctg tac atc ctc 782  
Ser His Ser Arg Leu Ser Pro Arg Lys Thr His Leu Leu Tyr Ile Leu  
225 230 235

agg ccc tct cggtg cag ctg taggggtggg gaccggggag cacctgcctg 830  
Arg Pro Ser Arg Gln Leu  
240

tagccccat cagaccctgc cccaaagcacc atatggaaat aaagttcttt cttacatcta 890  
aaaaaaaaaaaa aaaaaaaaaa aaaaaaaaaattg gccccccgc 928

*B*  
*Cmt*

<210> 14  
<211> 242  
<212> PRT  
<213> Homo sapiens

<400> 14  
Met Gly Glu Ala Ser Pro Pro Ala Pro Ala Arg Arg His Leu Leu Val  
1 5 10 15

Leu Leu Leu Leu Leu Ser Thr Leu Val Ile Pro Ser Ala Ala Ala Pro  
20 25 30

Ile His Asp Ala Asp Ala Gln Glu Ser Ser Leu Gly Leu Thr Gly Leu  
35 40 45

Gln Ser Leu Leu Gln Gly Phe Ser Arg Leu Phe Leu Lys Gly Asn Leu  
50 55 60

Leu Arg Gly Ile Asp Ser Leu Phe Ser Ala Pro Met Asp Phe Arg Gly  
65 70 75 80

Leu Pro Gly Asn Tyr His Lys Glu Glu Asn Gln Glu His Gln Leu Gly  
85 90 95

Asn Asn Thr Leu Ser Ser His Leu Gln Ile Asp Lys Met Thr Asp Asn  
100 105 110

Lys Thr Gly Glu Val Leu Ile Ser Glu Asn Val Val Ala Ser Ile Gln  
115 120 125

Pro Ala Glu Gly Ser Phe Glu Gly Asp Leu Lys Val Pro Arg Met Glu  
130 135 140

Glu Lys Glu Ala Leu Val Pro Ile Gln Lys Ala Thr Asp Ser Phe His  
145 150 155 160

Thr Glu Leu His Pro Arg Val Ala Phe Trp Ile Ile Lys Leu Pro Arg  
165 170 175

Arg Arg Ser His Gln Asp Ala Leu Glu Gly Gly His Trp Leu Ser Glu  
180 185 190

Lys Arg His Arg Leu Gln Ala Ile Arg Asp Gly Leu Arg Lys Gly Thr  
195 200 205

His Lys Asp Val Leu Glu Glu Gly Thr Glu Ser Ser Ser His Ser Arg  
210 215 220

Leu Ser Pro Arg Lys Thr His Leu Leu Tyr Ile Leu Arg Pro Ser Arg  
225 230 235 240

Gln Leu

*B1*  
*Cont.*

<210> 15  
<211> 726  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)..(726)

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atg gga gaa gcc tcc cca cct gcc ccc gca agg cgg cat ctg ctg gtc 48  
Met Gly Ala Ser Pro Pro Ala Pro Ala Arg Arg His Leu Leu Val  
1 5 10 15

ctg ctg ctg ctc ctc tct acc ctg gtg atc ccc tcc gct gca gct cct 96  
Leu Leu Leu Leu Ser Thr Leu Val Ile Pro Ser Ala Ala Ala Pro  
20 25 30

atc cat gat gct gac gcc caa gag agc tcc ttg ggt ctc aca ggc ctc 144  
Ile His Asp Ala Asp Ala Gln Glu Ser Ser Leu Gly Leu Thr Gly Leu  
35 40 45

cag agc cta ctc caa ggc ttc agc cga ctt ttc ctg aaa ggt aac aac 192  
Gln Ser Leu Leu Gln Gly Phe Ser Arg Leu Phe Leu Lys Gly Asn Leu  
50 55 60

ctt cgg ggc ata gac agc tta ttc tct gcc ccc atg gac ttc cgg ggc 240  
Leu Arg Gly Ile Asp Ser Leu Phe Ser Ala Pro Met Asp Phe Arg Gly  
65 70 75 80

ctc cct ggg aac tac cac aaa gag gag aac cag gag cac cag ctg ggg 288  
Leu Pro Gly Asn Tyr His Lys Glu Glu Asn Gln Glu His Gln Leu Gly  
85 90 95

aac aac acc ctc tcc agc cac ctc cag atc gac aag atg acc gac aac 336  
Asn Asn Thr Leu Ser Ser His Leu Gln Ile Asp Lys Met Thr Asp Asn  
100 105 110

aag aca gga gag gtg ctg atc tcc gag aat gtg gtg gca tcc att caa 384  
Lys Thr Gly Glu Val Leu Ile Ser Glu Asn Val Val Ala Ser Ile Gln  
115 120 125

cca gcg gag ggg agc ttc gag ggt gat ttg aag gta ccc agg atg gag 432  
Pro Ala Glu Gly Ser Phe Glu Gly Asp Leu Lys Val Pro Arg Met Glu  
130 135 140

gag aag gag gcc ctg gta ccc atc cag aag gcc acg gac agc ttc cac 480  
Glu Lys Glu Ala Leu Val Pro Ile Gln Lys Ala Thr Asp Ser Phe His  
145 150 155 160

aca gaa ctc cat ccc cgg gtg gcc ttc tgg atc att aag ctg cca cgg 528  
Thr Glu Leu His Pro Arg Val Ala Phe Trp Ile Ile Lys Leu Pro Arg  
165 170 175

cgg agg tcc cac cag gat gcc ctg gag ggc ggc cac tgg ctc agc gag 576  
Arg Arg Ser His Gln Asp Ala Leu Glu Gly Gly His Trp Leu Ser Glu  
180 185 190

*B1*  
*cont.*

aag cga cac cgc ctg cag gcc atc cgg gat gga ctc cgc aag ggg acc 624  
Lys Arg His Arg Leu Gln Ala Ile Arg Asp Gly Leu Arg Lys Gly Thr  
195 200 205

cac aag gac gtc cta gaa gag ggg acc gag agc tcc tcc cac tcc agg 672  
His Lys Asp Val Leu Glu Gly Thr Glu Ser Ser Ser His Ser Arg  
210 215 220

ctg tcc ccc cga aag acc cac tta ctg tac atc ctc agg ccc tct cgg 720  
Leu Ser Pro Arg Lys Thr His Leu Leu Tyr Ile Leu Arg Pro Ser Arg  
225 230 235 240

cag ctg  
Gln Leu 726

<210> 16  
<211> 2381  
<212> DNA  
<213> Homo sapiens

<220>

<221> CDS

<222> (110)..(1156)

<400> 16

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agctcagctt tgttcattcg aattggcg ggccagcgc ggaacaaac atg cag cgg 118  
Met Gln Arg  
1

ctc ggg ggt att ttg ctg tgt aca ctg ctg gcg gcg gcg gtc ccc act 166  
Leu Gly Gly Ile Leu Leu Cys Thr Leu Leu Ala Ala Ala Val Pro Thr  
5 10 15

gct cct gct cct tcc ccg acg gtc act tgg act ccg gcg gag ccg ggc 214  
Ala Pro Ala Pro Ser Pro Thr Val Thr Trp Thr Pro Ala Glu Pro Gly  
20 25 30 35

cca gct ctc aac tac cct cag gag gaa gct acg ctc aat gag atg ttt 262  
Pro Ala Leu Asn Tyr Pro Gln Glu Glu Ala Thr Leu Asn Glu Met Phe  
40 45 50

cga gag gtg gag gag ctg atg gaa gac act cag cac aaa ctg cgc agt 310  
Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys Leu Arg Ser  
55 60 65

gcc gtg gag gag atg gag gcg gaa gca gct gct aaa acg tcc tct 358  
Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys Thr Ser Ser  
70 75 80

gag gtg aac ctg gca agc tta cct ccc aac tat cac aat gag acc agc 406  
Glu Val Asn Leu Ala Ser Leu Pro Pro Asn Tyr His Asn Glu Thr Ser  
85 90 95

acg gag acc agg gtg gga aat aac aca gtc cat gtg cac cag gaa gtt 454  
Thr Glu Thr Arg Val Gly Asn Asn Thr Val His Val His Gln Glu Val  
100 105 110 115

cac aag ata acc aac cag agt gga cag gtg gtc ttt tct gag aca 502  
His Lys Ile Thr Asn Asn Gln Ser Gly Gln Val Val Phe Ser Glu Thr  
120 125 130

gtc att aca tct gta ggg gat gaa gaa ggc aag agg agc cat gaa tgt 550  
Val Ile Thr Ser Val Gly Asp Glu Glu Gly Lys Arg Ser His Glu Cys  
135 140 145

atc att gat gaa gac tgt ggg ccc acc agg tac tgc cag ttc tcc agc 598  
Ile Ile Asp Glu Asp Cys Gly Pro Thr Arg Tyr Cys Gln Phe Ser Ser  
150 155 160

ttc aag tac acc tgc cag cca tgc cgg gac cag cag atg cta tgc acc 646  
Phe Lys Tyr Thr Cys Gln Pro Cys Arg Asp Gln Gln Met Leu Cys Thr  
165 170 175

B  
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cga gac agt gag tgc tgt gga gac cag ctg tgt gcc tgg ggt cac tgc 694  
Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Ala Trp Gly His Cys  
180 185 190 195

acc caa aag gcc acc aaa ggt ggc aat ggg acc atc tgt gac aac cag 742  
Thr Gln Lys Ala Thr Lys Gly Gly Asn Gly Thr Ile Cys Asp Asn Gln  
200 205 210

agg gat tgc cag cct ggc ctg tgt tgt gcc ttc caa aga ggc ctg ctg 790  
Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg Gly Leu Leu  
215 220 225

ttc ccc gtg tgc aca ccc ctg ccc gtg gag gga gag ctc tgc cat gac 838  
Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu Cys His Asp  
230 235 240

ccc acc agc cag ctg ctg gat ctc atc acc tgg gaa ctg gag cct gaa 886  
Pro Thr Ser Gln Leu Leu Asp Leu Ile Thr Trp Glu Leu Glu Pro Glu  
245 250 255

gga gct ttg gac cga tgc ccc tgc gcc agt ggc ctc cta tgc cag cca 934  
Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu Cys Gln Pro  
260 265 270 275

cac agc cac agt ctg gtg tac atg tgc aag cca gcc ttc gtg ggc agc 982  
His Ser His Ser Leu Val Tyr Met Cys Lys Pro Ala Phe Val Gly Ser  
280 285 290

cat gac cac agt gag gag agc cag ctg ccc agg gag gcc ccg gat gag 1030  
His Asp His Ser Glu Glu Ser Gln Leu Pro Arg Glu Ala Pro Asp Glu  
295 300 305

tac gaa gat gtt ggc ttc ata ggg gaa gtg cgc cag gag ctg gaa gac 1078  
Tyr Glu Asp Val Gly Phe Ile Gly Glu Val Arg Gln Glu Leu Glu Asp  
310 315 320

ctg gag cgg agc cta gcc cag gag atg gca ttt gag ggg cct gcc cct 1126  
Leu Glu Arg Ser Leu Ala Gln Glu Met Ala Phe Glu Gly Pro Ala Pro  
325 330 335

gtg gag tca cta ggc gga gag gag gag att taggcccaga cccagctgag 1176  
Val Glu Ser Leu Gly Gly Glu Glu Glu Ile  
340 345

tcactggtag atgtgcaata gaaatggcta atttattttc ccaggagtgt ccccaagtgt 1236

ggaatggccg cagctcccttc ccagtagctt ttcctctggc ttgacaaggt acagtgcagt 1296

acattttcttc cagccgcctt gcttctctga cttggaaag acaggcatgg cgggttaaggg 1356

cagcggtgag tcgtccctcg ctgttgctag aaacgctgtc ttgttcttca tggatggaag 1416

atttgttga agggagagga tggaaagggg tgaagtctgc tcatgatgga tttggggat 1476

acagggagga ggtatgcctgc cttgcagacg tggacttggc aaaatgtaac ctttgcttt 1536

B1  
Cont.

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tgttagtac agctgtgaca tacagacaga agaaggctgg gctggatgtc aggcctcaga 2136  
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gaaagttgca cacatttcta taagcatgcc tttctcctga gttttaatt atatgtatac 2256  
acaaacatgt gcccctcaaa gatcatgcac aaaccactac tcttgctaa ttcttgact 2316  
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gcccgc 2381

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Glu Pro Gly Pro Ala Leu Asn Tyr Pro Gln Glu Glu Ala Thr Leu Asn  
35 40 45

Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys  
50 55 60

Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys  
65 70 75 80

Thr Ser Ser Glu Val Asn Leu Ala Ser Leu Pro Pro Asn Tyr His Asn  
85 90 95

Glu Thr Ser Thr Glu Thr Arg Val Gly Asn Asn Thr Val His Val His  
100 105 110

Gln Glu Val His Lys Ile Thr Asn Asn Gln Ser Gly Gln Val Val Phe  
115 120 125

Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Lys Arg Ser  
130 135 140

His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Thr Arg Tyr Cys Gln  
145 150 155 160

Phe Ser Ser Phe Lys Tyr Thr Cys Gln Pro Cys Arg Asp Gln Gln Met  
165 170 175

Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Ala Trp  
180 185 190

Gly His Cys Thr Gln Lys Ala Thr Lys Gly Gly Asn Gly Thr Ile Cys  
195 200 205

Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg  
210 215 220

Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu  
225 230 235 240

Cys His Asp Pro Thr Ser Gln Leu Leu Asp Leu Ile Thr Trp Glu Leu  
245 250 255

Glu Pro Glu Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu  
260 265 270

Cys Gln Pro His Ser His Ser Leu Val Tyr Met Cys Lys Pro Ala Phe  
275 280 285

Val Gly Ser His Asp His Ser Glu Glu Ser Gln Leu Pro Arg Glu Ala  
290 295 300

Pro Asp Glu Tyr Glu Asp Val Gly Phe Ile Gly Glu Val Arg Gln Glu  
305 310 315 320

Leu Glu Asp Leu Glu Arg Ser Leu Ala Gln Glu Met Ala Phe Glu Gly  
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1 5 10 15

gtc ccc act gct cct gct tcc ccg acg gtc act tgg act ccg gcg 96  
Val Pro Thr Ala Pro Ala Pro Ser Pro Thr Val Thr Trp Thr Pro Ala  
20 25 30

gag ccg ggc cca gct ctc aac tac cct cag gag gaa gct acg ctc aat 144  
Glu Pro Gly Pro Ala Leu Asn Tyr Pro Gln Glu Glu Ala Thr Leu Asn  
35 40 45

gag atg ttt cga gag gtg gag gag ctg atg gaa gac act cag cac aaa 192  
Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys  
50 55 60

ctg cgc agt gcc gtg gag gag atg gag gcg gaa gca gct gct aaa 240  
Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys  
65 70 75 80

acg tcc tct gag gtg aac ctg gca agc tta cct ccc aac tat cac aat 288  
Thr Ser Ser Glu Val Asn Leu Ala Ser Leu Pro Pro Asn Tyr His Asn  
85 90 95

gag acc agc acg gag acc agg gtg gga aat aac aca gtc cat gtg cac 336  
Glu Thr Ser Thr Glu Thr Arg Val Gly Asn Asn Thr Val His Val His  
100 105 110

cag gaa gtt cac aag ata acc aac aac cag agt gga cag cag gtg gtc ttt 384  
Gln Glu Val His Lys Ile Thr Asn Asn Gln Ser Gly Gln Val Val Phe  
115 120 125

tct gag aca gtc att aca tct gta ggg gat gaa gaa ggc aag agg agc 432  
Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Lys Arg Ser  
130 135 140

cat gaa tgt atc att gat gaa gac tgt ggg ccc acc agg tac tgc cag 480  
His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Thr Arg Tyr Cys Gln  
145 150 155 160

ttc tcc agc ttc aag tac acc tgc cag cca tgc cgg gac cag cag atg 528  
Phe Ser Ser Phe Lys Tyr Thr Cys Gln Pro Cys Arg Asp Gln Gln Met  
165 170 175

cta tgc acc cga gac agt gag tgc tgt gga gac cag ctg tgt gcc tgg 576  
Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Ala Trp  
180 185 190

ggt cac tgc acc caa aag gcc acc aaa ggt ggc aat ggg acc atc tgt 624  
Gly His Cys Thr Gln Lys Ala Thr Lys Gly Gly Asn Gly Thr Ile Cys  
195 200 205

B  
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gac aac cag agg gat tgc cag cct ggc ctg tgt tgt gcc ttc caa aga	672		
Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg			
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ggc ctg ctg ttc ccc gtg tgc aca ccc ctg ccc gtg gag gga gag ctc	720		
Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu			
225	230	235	240
tgc cat gac ccc acc agc cag ctg ctg gat ctc atc acc tgg gaa ctg	768		
Cys His Asp Pro Thr Ser Gln Leu Leu Asp Leu Ile Thr Trp Glu Leu			
245	250	255	
gag cct gaa gga gct ttg gac cga tgc ccc tgc gcc agt ggc ctc cta	816		
Glu Pro Glu Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu			
260	265	270	
tgc cag cca cac agc cac agt ctg gtg tac atg tgc aag cca gcc ttc	864		
Cys Gln Pro His Ser His Ser Leu Val Tyr Met Cys Lys Pro Ala Phe			
275	280	285	
gtg ggc agc cat gac cac agt gag gag agc cag ctg ccc agg gag gcc	912		
Val Gly Ser His Asp His Ser Glu Glu Ser Gln Leu Pro Arg Glu Ala			
290	295	300	
ccg gat gag tac gaa gat gtt ggc ttc ata ggg gaa gtg cgc cag gag	960		
Pro Asp Glu Tyr Glu Asp Val Gly Phe Ile Gly Glu Val Arg Gln Glu			
305	310	315	320
ctg gaa gac ctg gag cgg agc cta gcc cag gag atg gca ttt gag ggg	1008		
Leu Glu Asp Leu Glu Arg Ser Leu Ala Gln Glu Met Ala Phe Glu Gly			
325	330	335	
cct gcc cct gtg gag tca cta ggc gga gag gag gag att	1047		
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